Amendments to the Claims

1. (Currently Amended) A method of [~~modulating~~] promoting hematopoietic stem cell differentiation, comprising:

contacting [~~said~~] hematopoietic stem cells *in vitro* with one or more antisense morpholino oligomers[,] having a substantially uncharged backbone and a base sequence directed to a target sequence spanning the translational start codon or an intron or exon junction site of an mRNA [~~preferentially expressed in stem cells~~] transcribed from a human EVI-1 zinc finger gene,

wherein said contacting is effective to achieve (i) an increase in the number of lineage committed progenitor cells and their progeny, and/or (ii) a slowing or diminution of the growth of cells exhibiting a loss of growth control, or a reduction in the total number of such cells.

2. (Cancelled)

3. (Previously amended) The method of claim 1, wherein each of said one or more antisense oligomers has a length of about 12 to 25 bases.

4. (Previously amended) The method of claim 1, wherein each of said one or more antisense oligomers is characterized by

(a) a backbone which is substantially uncharged;

(b) the ability to hybridize with the complementary sequence of a target RNA with high affinity at a Tm greater than 50°C;

(c) nuclease resistance; and

(d) the capability for active or facilitated transport into cells.

5. (Previously amended) The method of claim 1, wherein said antisense morpholino oligomer comprises phosphorodiamidate intersubunit linkages, joining a morpholino nitrogen of one morpholino subunit to a 5'-exocyclic carbon of an adjacent morpholino subunit.

6. (Currently Amended) The method according to claim [2] 1, wherein each of said one or more antisense oligomers has [a sequence selected from the group consisting of] the sequence presented as SEQ ID NO:1[, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:10, SEQ ID NO:11 and SEQ ID NO:12].

7-9. (Cancelled)

10. (Currently Amended) [A method of modulating hematopoietic stem cell differentiation, comprising:] The method of claim 1, wherein said hematopoietic stem cells are provided by:

(a) obtaining a stem cell-containing cell population from a subject; and

(b) treating the cell population in manner effective to enrich the cell population for stem cells[; and

(c) exposing the enriched stem cell population *ex vivo* to one or more antisense morpholino oligomers, having a substantially uncharged backbone and a base sequence directed to a target sequence spanning the translational start codon or an intron or exon junction site of an mRNA preferentially expressed in stem cells,

under conditions effective to (i) to increase the population of lineage committed progenitor cells and their progeny in the peripheral circulation of the subject, and/or (ii) effect a slowing or diminution of the growth of cells exhibiting a loss of growth control, or a reduction in the total number of such cells; and

(d) infusing the antisense oligomer-treated cell population into said subject].

11-16. (Cancelled)

17. (Currently Amended) A composition comprising an antisense morpholino oligomer characterized by a backbone which is substantially uncharged, where said oligomer is directed to a sequence spanning the mRNA translational start codon of a human EVI-1 zinc finger gene [preferentially expressed in stem cells].

18. (Cancelled)

19. (Currently Amended) A composition comprising an antisense oligomer having an [~~substantially~~] uncharged backbone, wherein said antisense oligomer is characterized by

(a) the ability to hybridize with the complementary sequence of a target RNA with high affinity at a Tm greater than 50°C,

(b) nuclease resistance, and

(c) the capability for active or facilitated transport into cells;

and has the sequence presented as SEQ ID NO:1.

20. (Cancelled)

21. (New) The method of claim 10, further comprising the step of infusing the antisense oligomer-treated cell population into said subject.

22. (New) The composition of claim 17, wherein said oligomer has the base sequence presented as SEQ ID NO:1.